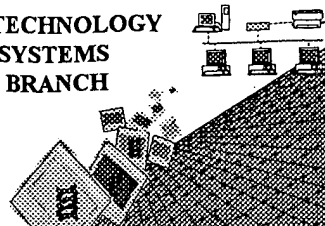# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _10/009,705A_

Source: _Py/10_

Date Processed by STIC: _7/25/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: **patin21help@uspto.gov** or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: **patin3help@uspto.gov** or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>** , **EFS Submission User Manual - ePAVE**)
2. **U.S. Postal Service:** U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. **Hand Carry directly to:**
    U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
        Or
    U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
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Revised 01/29/2002

PCT10

RAW SEQUENCE LISTING   DATE: 07/25/2002
PATENT APPLICATION: US/10/009,705A   TIME: 11:19:02

Input Set : A:\seilpct-US-seqp-neu.txt
Output Set: N:\CRF3\07252002\J009705A.raw

Does Not Comply
Corrected Diskette Needed

```
 2 <110> APPLICANT: Ruprecht-Karls-Universit,t Heidelberg
 4 <120> TITLE OF INVENTION: Method for the specific detection and identification
 5        of retroviral nucleic acids/retroviruses in a specimen
 7 <130> FILE REFERENCE: seilpct-US
 9 <140> CURRENT APPLICATION NUMBER: US/10/009,705A
10 <141> CURRENT FILING DATE: 2002-05-28
12 <150> PRIOR APPLICATION NUMBER: DE 199 21 419.0
13 <151> PRIOR FILING DATE: 1999-05-08 ·
15 <160> NUMBER OF SEQ ID NOS: 4
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 18
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
23 <220> FEATURE: highly degenerate artificial oligonucleotide sequence
23 <220> FEATURE: highly degenerate artificial oligonucleotide sequence
24 <223> OTHER INFORMATION: primer sequence allows amplification of reverse
25        transcriptase-related sequences by multiplex PCR
27 <400> SEQUENCE: 1
28 aragnytdy chcmrggh                                              18
31 <210> SEQ ID NO: 2
32 <211> LENGTH: 18
33 <212> TYPE: DNA
34 <213> ORGANISM: Homo sapiens
35 <220> FEATURE: highly degenerate artificial oligonucleotide sequence
36 <220> FEATURE: highly degenerate artificial oligonucleotide sequence
36 <223> OTHER INFORMATION: primer sequence allows amplification of reverse
37        transcriptase-related sequences by multiplex PCR
39 <400> SEQUENCE: 2
40 nwddmkdtya tcmayrwa                                             18
43 <210> SEQ ID NO: 3
44 <211> LENGTH: 21
45 <212> TYPE: DNA
46 <213> ORGANISM: Homo sapiens
47 <220> FEATURE: highly degenerate artificial oligonucleotide sequence
47 <220> FEATURE: highly degenerate artificial oligonucleotide sequence
48 <223> OTHER INFORMATION: primer sequence allows amplification of reverse
49        transcriptase-related sequences by multiplex PCR
51 <400> SEQUENCE: 3
52 tkkammskvy trcyhcargg g                                         21
55 <210> SEQ ID NO: 4
56 <211> LENGTH: 21
57 <212> TYPE: DNA
```

Handwritten annotations:
Per 1.823 of Sequence Rules, do not insert a response to <2207. <2207 is a "leader" only. Explain <213> response on <223> line.

see p. 3 for explanation (×2)

same error

same

W--> (marginal marks beside lines 23, 23, 28, 35, 36, 40, 47, 47)

RAW SEQUENCE LISTING
PATENT APPLICATION: **US/10/009,705A**

DATE: 07/25/2002
TIME: 11:19:02

Input Set : **A:\seilpct-US-seqp-neu.txt**
Output Set: **N:\CRF3\07252002\J009705A.raw**

```
       58 <213> ORGANISM: Homo sapiens
W-->   59 <220> FEATURE: highly degenerate artificial oligonucleotide sequence
W-->   59 <220> FEATURE: highly degenerate artificial oligonucleotide sequence    same
       60 <223> OTHER INFORMATION: primer sequence allows amplification of reverse    error
       61        transcriptase-related sequences by multiplex PCR
       63 <400> SEQUENCE: 4
       64 mdvhdrbmdk ymayvyahkk a                                    21
```

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/009,705A

DATE: 07/25/2002
TIME: 11:19:03

Input Set : A:\seilpct-US-seqp-neu.txt
Output Set: N:\CRF3\07252002\J009705A.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 6
Seq#:2; N Pos. 1

Input Set : **A:\seilpct-US-seqp-neu.txt**
Output Set: **N:\CRF3\07252002\J009705A.raw**

L:9 M:270 C: Current Application Number differs, Replaced Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:23 M:283 W: Missing Blank Line separator, <220> field identifier
L:23 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:28 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:28 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:28 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:35 M:283 W: Missing Blank Line separator, <220> field identifier
L:35 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:40 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:40 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:40 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:47 M:283 W: Missing Blank Line separator, <220> field identifier
L:47 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:59 M:283 W: Missing Blank Line separator, <220> field identifier
L:59 M:256 W: Invalid Numeric Header Field, <220> has non-blank data